IN THE CLAIMS

1. (Currently Amended) A method for specific genotyping, typing, identification, detection or sequencing of nucleic acid molecules comprising:

a) providing a sample containing nucleic acid molecules which are suspected to contain at least one type or species or target of a variable region, region of interest or target DNA, each type or species or target having different nucleotide patterns;

b) providing a mixed pool of at least two structurally different sequencing oligonucleotide primers, whereby each primer is designed for being specific for one type or species or group or target chosen from the known set of types or target of the nucleic acid sample, thereby allowing a primer, which is specific for a type, species, group or target that is present in the sample, to hybridize in or close to the target or variable region;

c) mixing the sample and mixed pool of specific primers under conditions allowing a primer or primers to hybridize if a target type or types are present in the sample; and

d) determining the type, species or target region to which the primer or primers have hybridized by extending the hybridized primer or primers ~~in a DNA~~ using Sanger sequencing ~~reaction~~, pyrosequencing or mass spectrometry DNA sequencing.

2. (Previously Presented) The method according to claim 1, wherein the sequencing reaction is performed by sequencing-by-synthesis, Sanger dideoxy sequencing, sequencing by mass spectrometry or any other DNA sequencing technology, applicable to the method of invention.

3. (Previously Presented) The method according to claim 2, wherein the sample is a microorganism, virus, fungi or bacteria.

4. (Previously Presented) The method according to claim 3, wherein the sample is suspected to comprise at least two types, species or targets of nucleic acid molecules chosen from the known set of types, species or targets.

5. (Previously Presented) The method according to claim 4, wherein the sample contains multiple infection or variants or types or species.

6. (Previously Presented) The method according to claim 5, wherein at least one primer is specific for a variant of a disease linked to the microorganism.

7. (Previously Presented) The method according to claim 6, wherein the microorganism is a human papillomavirus

8. (Previously Presented) The method according to claim 7, wherein the known set of HPV-types are chosen from the group comprising the HPV-types; high-risk: 16, 18, 31, 33, 35, 39, 45, 51, 52, 58, 59, 66, 68, 69 and low-risk: 6, 11, 34, 40, 42, 43, 44

9. (Previously Presented) The method according to claim 8, wherein semi-conservative regions are sequenced.

10. (Previously Presented) The method according to claim 9, wherein amplicons comprising at least one semi-conservative region are typed.

11. (Previously Presented) The method according to claim 10, wherein samples possessing a minority type or species or possessing a low yield amplification fragment are typed.

12. (Currently Amended) The method according to claim 11, wherein samples that contain unspecific amplification products are not typed by DNA sequencing, and wherein the primers in the set of primers do not anneal to unspecific amplification products.

13. (Withdrawn) Kit for use in the method of typing of claim 1-12, comprising at least two oligonucleotide primers, whereby each primer is designed for being specific for one genotype or type or species or group or target or type-specific region chosen from a

known set of types of the type-specific or target region of a nucleic acid sample, thereby allowing a primer, which is specific for a genotype or type or species or target that is present in the sample, to hybridize in or close to the type-specific or target region.

14. (Withdrawn) Kit according to claim 13, wherein the oligonucleotide primers of the kit are designed for being specific for any of the HPV-types chosen from the group comprising: high-risk: HPV-16, 18, 31, 33, 35, 39, 45, 51, 52, 58, 59, 66, 68, 69 and low-risk: HPV-6, 11, 34, 40, 42, 43, 44

15. (Withdrawn) Kit according to any one of the preceding claims for genotyping, typing, detection, identification or sequencing of any microorganisms, viruses or any other application where the multiple sequencing oligonucleotide primer pool approach is applicable by DNA sequencing technologies

16. (Withdrawn) Kit according to claim 1 for quantitative measurements of different genotypes or species or types amplified by PCR in the same sample or by mixing different amplicons